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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/846,456	05/02/2001	Marie-Francoise Rosier-Montus	ST00015 US NP	1457
5487	7590	07/31/2007		
ROSS J. OEHLER SANOFI-AVENTIS U.S. LLC 1041 ROUTE 202-206 MAIL CODE: D303A BRIDGEWATER, NJ 08807			EXAMINER SULLIVAN, DANIEL M	
			ART UNIT 1636	PAPER NUMBER
			NOTIFICATION DATE 07/31/2007	DELIVERY MODE ELECTRONIC

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

USPatent.E-Filing@sanofi-aventis.com
andrea.ryan@sanofi-aventis.com

Office Action Summary	Application No. 09/846,456	Applicant(s) ROSIER-MONTUS ET AL.	
	Examiner Daniel M. Sullivan	Art Unit 1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 12 July 2007.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1,3,7-12,33-36 and 57-60 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1,3,33-36 and 57-60 is/are rejected.
- 7) ☒ Claim(s) 7-12 is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)
Paper No(s)/Mail Date _____ | 6) <input checked="" type="checkbox"/> Other: <u>See Continuation Sheet</u> . |

Continuation of Attachment(s) 6). Other: SEQUENCE SEARCH RESULTS 09/846,456.

DETAILED ACTION

This Office Action is a reply to the Paper filed 12 July 2007 in response to the Non-Final Office Action mailed 14 February 2007. Claims 1-3, 5-14, 33-38, 57-60 were considered in the 14 February Office Action. Claims 2, 5, 6, 37 and 38 were cancelled in the 12 July Paper. Claims 1, 3, 7-12, 33-36 and 57-60 are pending and under consideration. Finality of the previous Office Action is withdrawn in view of the new grounds for rejection set forth herein below.

Response to Amendment and Arguments

Rejection of claims 2, 5, 6, 37 and 38 is rendered moot by the cancellation thereof.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Rejection of claim 10 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite in reciting, "ranging from nucleotide 1 at position -1" is withdrawn in view of the claim amendment.

New Grounds

Claim Objections

Claim 57 is objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the

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claim(s) in independent form. Claim 57 is directed to the isolated nucleic acid of claim 1, comprising at least 20 consecutive nucleotides of the sequence SEQ ID NO: 3 or the complement of SEQ ID NO: 3. Claim 1 is directed to an isolated nucleic acid comprising 500 or more consecutive nucleotides of SEQ ID NO: 1 or the complement of SEQ ID NO: 1.

As shown in the alignment of SEQ ID NO: 1 and SEQ ID NO: 3 attached hereto (us-09-846-456a-1.rnpbm, RESULT 7; page 8), SEQ ID NO: 3 comprises all but the final 338 bases of SEQ ID NO: 1. Therefore, any sequence comprising 500 or more consecutive nucleotides of SEQ ID NO: 1 must, at a minimum, comprise 162 bases of SEQ ID NO: 3. Therefore, all sequences within the scope of claim 1 must comprise more than 20 bases of SEQ ID NO: 3 and, consequently, claim 57 fails to further limit the subject matter of claim 1.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

Claims 1, 3, 33-36 and 57-60 are rejected under 35 U.S.C. 102(a) as being anticipated by NCBI Entrez Nucleotide Database entry AC012230.2 (19 November 1999), <http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=6454033>, downloaded 25 July 2007 as evidenced by Osoegawa et al. (2001) *Genome Res.* 11:483-496.

Claim 1 is directed to an isolated nucleic acid comprising a polynucleotide having 500 or more consecutive nucleotides of the nucleotide sequence SEQ ID NO: 1 and claim 3 is directed

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to an isolated nucleic acid comprising a polynucleotide having at least 200 consecutive nucleotides of the sequence SEQ ID NO: 3. Claim 57 is directed to the nucleic acid of claim 1, wherein the nucleic acid comprises at least 20 consecutive nucleotides of SEQ ID NO: 3.

The AC012230 entry teaches a nucleic acid comprising a 540 base sequence that is identical to nucleotides 2130-2670 of SEQ ID NO: 1 and 3. (See the alignment of SEQ ID NO: 3 with the AC012230 entry on the attached sequence search results (us-09-846-456a-3.oli.rge, RESULT 11). Note that the sequence at nucleotides 2130-2670 of SEQ ID NO: 1 is identical to the sequence of SEQ ID NO: 3 (see us-09-846-456a-1.rnpbm, RESULT 7; page 8 of the attached sequence search). Also note that the alignment on the sequence search is numbered according to version 3 of the AC012230 entry while the cited art is version 2 (i.e., AC012230.2). The corresponding sequence begins at 2703 and continues through 3243 of the AC012230.2 sequence.

The AC012230 entry anticipates the limitations of the instant claims 1, 3 and 57. In addition, the AC012230 nucleic acid further comprises additional sequence which is "of interest" according to the limitations of claim 33 and would additionally comprise sequence that is in the sense and antisense orientation with respect to the promoter comprised by the nucleic acid, as well as sense and antisense sequences of interest comprised by the BAC vector itself, according to the limitations of claim 34. Claim 58 recites that the isolated nucleic acid further comprises 35 or more consecutive nucleotides of SEQ ID NO: 5 or the complement of SEQ ID NO: 5. This limitation is met by, for example, the sequence from 147555-147614 of the AC012230.2 sequence, which is 100% complementary to the sequence from nucleotide 100 to nucleotide 159 of SEQ ID NO: 5.

Finally, the AC012230 entry teaches that the sequence is comprised in an RP11 clone (a.k.a., RPC-11; see under "DEFINITION"). Osoegawa et al. teaches that RPCI-11 is a BAC library. (See especially page 492, second sentence of the "DISCUSSION".) In view of the fact that nucleic acids in BAC libraries are comprised within vectors and propagated in bacteria, the cloning vector of claims 35 and 36 and isolated host cell of claims 59 and 60 are inherent to the teaching of the nucleic acid comprised in an RP11 clone as disclosed in the AC012230.

Database entry AC012230, as evidenced by Osoegawa et al., teaches all of the limitations of the instant claims. Therefore, the claims are anticipated by the prior art.

Allowable Subject Matter

Claims 7-12 are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Daniel M. Sullivan whose telephone number is 571-272-0779. The examiner can normally be reached on Monday through Friday 6:30-3:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Joseph Woitach, Ph.D. can be reached on 571-272-0739. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) (<http://pair->

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direct.uspto.gov) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.



Daniel M. Sullivan, Ph.D.
Primary Examiner
Art Unit 1636

SEQUENCE SEARCH RESULTS 09/846,456

us-09-846-456a-3.oli.rge

RESULT 11

AC012230

LOCUS AC012230 175064 bp DNA linear HTG 22-APR-2000

DEFINITION Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered pieces.

ACCESSION AC012230

VERSION AC012230.3 GI:7637254

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 175064)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens, clone RP11-1M10

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 175064)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

TITLE Direct Submission

JOURNAL Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On Apr 22, 2000 this sequence version replaced gi:6454033.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L2510

Center clone name: 1_M_10

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 117571 bases at least Q40

Consensus quality: 145749 bases at least Q30

Consensus quality: 160940 bases at least Q20

Insert size: 185000; agarose-fp

Insert size: 171264; sum-of-contigs

Quality coverage: 2.9 in Q20 bases; agarose-fp

Quality coverage: 3.2 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 39 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1003: contig of 1003 bp in length

*	1004	1103: gap of 100 bp
*	1104	2634: contig of 1531 bp in length
*	2635	2734: gap of 100 bp
*	2735	4415: contig of 1681 bp in length
*	4416	4515: gap of 100 bp
*	4516	5785: contig of 1270 bp in length
*	5786	5885: gap of 100 bp
*	5886	7879: contig of 1994 bp in length
*	7880	7979: gap of 100 bp
*	7980	9686: contig of 1707 bp in length
*	9687	9786: gap of 100 bp
*	9787	12253: contig of 2467 bp in length
*	12254	12353: gap of 100 bp
*	12354	15228: contig of 2875 bp in length
*	15229	15328: gap of 100 bp
*	15329	17200: contig of 1872 bp in length
*	17201	17300: gap of 100 bp
*	17301	20131: contig of 2831 bp in length
*	20132	20231: gap of 100 bp
*	20232	22587: contig of 2356 bp in length
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*	97902	98001: gap of 100 bp
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*	124080	124179: gap of 100 bp
*	124180	131281: contig of 7102 bp in length
*	131282	131381: gap of 100 bp
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*	138060	138159: gap of 100 bp

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* 138160 145491: contig of 7332 bp in length
* 145492 145591: gap of 100 bp
* 145592 157391: contig of 11800 bp in length
* 157392 157491: gap of 100 bp
* 157492 175064: contig of 17573 bp in length.
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     misc_feature      56693. .59635
                        /note="assembly_fragment"
     misc_feature      59736. .63661
                        /note="assembly_fragment"
     misc_feature      63762. .68437
                        /note="assembly_fragment"
     misc_feature      68538. .71458
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                        vector_side:left"

Query Match      18.7%; Score 541; DB 2; Length 175064;
Best Local Similarity 100.0%; Pred. No. 2.4e-294;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2130 TTTGTTTGTTCCTTTTTTTGTTTTTGTGGCCTCCTTCCTCTCAATTTATGAAGAGAAGCA 2189
          |||

```

Db 2903 TTTGTTTGTCTCTTTTTTTGTTTTGTGGCCTCCTTCCTCTCAATTTATGAAGAGAAGCA 2962

Qy 2190 GTAAGATGTTCTCTCGGGTCTCTGAGGGACCTGGGGAGCTCAGGCTGGGAATCTCCAA 2249
 |||

Db 2963 GTAAGATGTTCTCTCGGGTCTCTGAGGGACCTGGGGAGCTCAGGCTGGGAATCTCCAA 3022

Qy 2250 GGCAGTAGGTGCGCTATCAAAAATCAAAGTCCAGGTTTGTGGGGGAAAACAAAAGCAGC 2309
 |||

Db 3023 GGCAGTAGGTGCGCTATCAAAAATCAAAGTCCAGGTTTGTGGGGGAAAACAAAAGCAGC 3082

Qy 2310 CCATTACCCAGAGGACTGTCCGCCTTCCCCTCACCCAGCCTAGGCCTTTGAAAGGAAAC 2369
 |||

Db 3083 CCATTACCCAGAGGACTGTCCGCCTTCCCCTCACCCAGCCTAGGCCTTTGAAAGGAAAC 3142

Qy 2370 AAAAGACAAGACAAAATGATTGGCGTCTGAGGGAGATTACGCTAGAGCTCTCTCTCCC 2429
 |||

Db 3143 AAAAGACAAGACAAAATGATTGGCGTCTGAGGGAGATTACGCTAGAGCTCTCTCTCCC 3202

Qy 2430 CCAATCCCTCCCTCCGGCTGAGGAACTAACAAAGGAAAAAAAAAATTGCGGAAAGCAGGA 2489
 |||

Db 3203 CCAATCCCTCCCTCCGGCTGAGGAACTAACAAAGGAAAAAAAAAATTGCGGAAAGCAGGA 3262

Qy 2490 TTTAGAGGAAGCAAATTCCTGCTGGTGCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCT 2549
 |||

Db 3263 TTTAGAGGAAGCAAATTCCTGCTGGTGCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCT 3322

Qy 2550 GCGGCGCAGCCCCGAGCCAGCGCTTCCCGCGCGTCTTAGGCCGCGGGCCCGGGCGGGG 2609
 |||

Db 3323 GCGGCGCAGCCCCGAGCCAGCGCTTCCCGCGCGTCTTAGGCCGCGGGCCCGGGCGGGG 3382

Qy 2610 GAAGGGGACGCAGACCGCGGACCCTAAGACACCTGCTGTACCCTCCACCCCCACCCACC 2669
 |||

Db 3383 GAAGGGGACGCAGACCGCGGACCCTAAGACACCTGCTGTACCCTCCACCCCCACCCACC 3442

Qy 2670 C 2670
 |

Db 3443 C 3443

~~6409-848456A/4. HADP~~

RESULT 12
 AC012230/c
 LOCUS AC012230 175064 bp DNA linear HTG 22-APR-2000
 DEFINITION Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
 pieces.
 ACCESSION AC012230
 VERSION AC012230.3 GI:7637254
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 175064)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens, clone RP11-1M10
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 175064)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
 Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
 Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
 Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
 Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
 Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
 Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
 McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
 Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,

TITLE
JOURNAL
COMMENT

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Apr 22, 2000 this sequence version replaced gi:6454033.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L2510

Center clone name: 1_M_10

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 117571 bases at least Q40

Consensus quality: 145749 bases at least Q30

Consensus quality: 160940 bases at least Q20

Insert size: 185000; agarose-fp

Insert size: 171264; sum-of-contigs

Quality coverage: 2.9 in Q20 bases; agarose-fp

Quality coverage: 3.2 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 39 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1003: contig of 1003 bp in length
* 1004 1103: gap of 100 bp
* 1104 2634: contig of 1531 bp in length
* 2635 2734: gap of 100 bp
* 2735 4415: contig of 1681 bp in length
* 4416 4515: gap of 100 bp
* 4516 5785: contig of 1270 bp in length
* 5786 5885: gap of 100 bp
* 5886 7879: contig of 1994 bp in length
* 7880 7979: gap of 100 bp
* 7980 9686: contig of 1707 bp in length
* 9687 9786: gap of 100 bp
* 9787 12253: contig of 2467 bp in length
* 12254 12353: gap of 100 bp
* 12354 15228: contig of 2875 bp in length
* 15229 15328: gap of 100 bp
* 15329 17200: contig of 1872 bp in length
* 17201 17300: gap of 100 bp
* 17301 20131: contig of 2831 bp in length
* 20132 20231: gap of 100 bp
* 20232 22587: contig of 2356 bp in length
* 22588 22687: gap of 100 bp
* 22688 25707: contig of 3020 bp in length
* 25708 25807: gap of 100 bp
* 25808 28184: contig of 2377 bp in length
* 28185 28284: gap of 100 bp
* 28285 31338: contig of 3054 bp in length
* 31339 31438: gap of 100 bp
* 31439 34299: contig of 2861 bp in length
* 34300 34399: gap of 100 bp
* 34400 38318: contig of 3919 bp in length
* 38319 38418: gap of 100 bp
* 38419 42835: contig of 4417 bp in length

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* 42836 42935: gap of 100 bp
* 42936 45448: contig of 2513 bp in length
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* 48217 52618: contig of 4402 bp in length
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* 59736 63661: contig of 3926 bp in length
* 63662 63761: gap of 100 bp
* 63762 68437: contig of 4676 bp in length
* 68438 68537: gap of 100 bp
* 68538 71458: contig of 2921 bp in length
* 71459 71558: gap of 100 bp
* 71559 76888: contig of 5330 bp in length
* 76889 76988: gap of 100 bp
* 76989 82113: contig of 5125 bp in length
* 82114 82213: gap of 100 bp
* 82214 88220: contig of 6007 bp in length
* 88221 88320: gap of 100 bp
* 88321 93499: contig of 5179 bp in length
* 93500 93599: gap of 100 bp
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* 97902 98001: gap of 100 bp
* 98002 103016: contig of 5015 bp in length
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* 103117 109178: contig of 6062 bp in length
* 109179 109278: gap of 100 bp
* 109279 117307: contig of 8029 bp in length
* 117308 117407: gap of 100 bp
* 117408 124079: contig of 6672 bp in length
* 124080 124179: gap of 100 bp
* 124180 131281: contig of 7102 bp in length
* 131282 131381: gap of 100 bp
* 131382 138059: contig of 6678 bp in length
* 138060 138159: gap of 100 bp
* 138160 145491: contig of 7332 bp in length
* 145492 145591: gap of 100 bp
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Query Match      11.9%; Score 344; DB 2; Length 175064;
Best Local Similarity 99.7%; Pred. No. 1.3e-182;
Matches 394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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us-09-846-456a-1.rnpbm

RESULT 7

US-09-846-456-3

; Sequence 3, Application US/09846456

; Patent No. US20020146792A1

; GENERAL INFORMATION:

; APPLICANT: Rosier, Marie

; APPLICANT: Prades, Catherine

; APPLICANT: Lemoine, Cendrine

; APPLICANT: Naudin, Laurent

; APPLICANT: Denefle, Patrice

; APPLICANT: Duverger, Nicolas

; APPLICANT: Brewer, Bryan

; APPLICANT: Remaley, Alan

; APPLICANT: Fojo, Silvia

; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying Its

; TITLE OF INVENTION: Activity and Therapeutic Uses

; FILE REFERENCE: 3806.0505

; CURRENT APPLICATION NUMBER: US/09/846,456

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/201,280

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 2893

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-846-456-3

Query Match 89.5%; Score 2893; DB 3; Length 2893;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1141	TCATCATGTTGGCCAGGTTGGTTTCGAACCTCTGACCTGAGGTGAGCTGCCACCTTGGC	1200
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          ||||||||||||||||||||||||||||||||||||||||
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Db      2881  CGGCAAAAACCCC 2893

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